# STIC Biotechnology Systems Branch

# RAW SEQUENCE LISTING
## ERROR REPORT

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:**

Application Serial Number: _/0/533,844A_

Source: _IFWP_

Date Processed by STIC: _8/4/06_

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**
**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
**http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio **(<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

# Raw Sequence Listing Error Summary

**ERROR DETECTED**      **SUGGESTED CORRECTION**      SERIAL NUMBER: _10/533, 8444A_

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1_____Wrapped Nucleics
      Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line **not exceed 72** characters in length. This includes white spaces.

3_____Misaligned Amino
      Numbering

The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4_____Non-ASCII

The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5_____Variable Length

Sequence(s)_____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
      "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7_____Skipped Sequences
      (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)        SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped  sequences.

8_____Skipped Sequences
      (NEW RULES)

Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
      (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10_____Invalid <213>
       Response

Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11_____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12_____PatentIn 2.0
       "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n/Xaa

"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – STIC Systems Branch – 03/02/06

IFWP

RAW SEQUENCE LISTING          DATE: 08/04/2006
PATENT APPLICATION:  US/10/533,844A      TIME: 13:15:18

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\08042006\J533844A.raw

```
 3 <110> APPLICANT: HAGEN, Frederick S.
 4        LANNFELT, Lars
 5        GELLERFORS, Par
 7 <120> TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF AGENTS THAT MODULATE THE
STRUCTURE AND
 8        PROCESSING OF BETA-AMYLOID PRECURSOR PROTEIN
10 <130> FILE REFERENCE: 017881-001010US
12 <140> CURRENT APPLICATION NUMBER: 10/533,844A
13 <141> CURRENT FILING DATE: 2005-05-04
15 <150> PRIOR APPLICATION NUMBER: PCT/2003/035294
16 <151> PRIOR FILING DATE: 2003-11-04
18 <160> NUMBER OF SEQ ID NOS: 5
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 8
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Leader Sequence
30 <400> SEQUENCE: 1
32 Asp Leu Tyr Asp Asp Asp Asp Lys
33 1               5
36 <210> SEQ ID NO: 2
37 <211> LENGTH: 11
38 <212> TYPE: PRT
39 <213> ORGANISM: Artificial Sequence
41 <220> FEATURE:
42 <223> OTHER INFORMATION: myc epitope
44 <400> SEQUENCE: 2
46 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
47 1               5                   10
50 <210> SEQ ID NO: 3
51 <211> LENGTH: 14
52 <212> TYPE: PRT
53 <213> ORGANISM: Artificial Sequence
55 <220> FEATURE:
56 <223> OTHER INFORMATION: v5 Epitope
58 <400> SEQUENCE: 3
60 Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr
61 1               5                   10
64 <210> SEQ ID NO: 4
65 <211> LENGTH: 8
66 <212> TYPE: PRT
67 <213> ORGANISM: Artificial Sequence
```

*see pp 1-3*

*insufficient response - give source of genetic material (see item 11 on Error Summary Sheet)*

Does Not Comply
Corrected Diskette Needed

OK

OK

RAW SEQUENCE LISTING           DATE: 08/04/2006
PATENT APPLICATION: US/10/533,844A    TIME: 13:15:18

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\08042006\J533844A.raw

```
69 <220> FEATURE:
70 <223> OTHER INFORMATION: the FLAG tag
72 <400> SEQUENCE: 4
74 Asp Tyr Lys Asp Asp Asp Asp Lys
75 1                   5
78 <210> SEQ ID NO: 5
79 <211> LENGTH: 5
80 <212> TYPE: PRT
81 <213> ORGANISM: Artificial Sequence
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Factor Xa amino acid substrate sequence
86 <220> FEATURE:
87 <221> NAME/KEY: MISC_FEATURE
88 <222> LOCATION: (5)..(5)
89 <223> OTHER INFORMATION: X=any amino acid
92 <400> SEQUENCE: 5
94 Ile Glu Gly Arg Xaa
95 1                   5
```

W-->

RAW SEQUENCE LISTING ERROR SUMMARY          DATE: 08/04/2006
PATENT APPLICATION:   US/10/533,844A          TIME: 13:15:19

*FYI*

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\08042006\J533844A.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 5

*FYI*

<u>Invalid Line Length:</u>
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7

**VERIFICATION SUMMARY**                    DATE: 08/04/2006
PATENT APPLICATION:  US/10/533,844A       TIME: 13:15:19

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\08042006\J533844A.raw**

L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0